



## eTBLAST: a text-similarity based search engine

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### Analyze the results with a post-processor:

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### Most Similar Matches in MEDLINE:

Score of self comparison: 103.997

- |    |   |                            |
|----|---|----------------------------|
| 1  | <a href="#">DNA amplification method tolerant to sample degradation.</a>  | Score: 94.2<br>Ratio:0.91  |
|    | G Wang, E Maher, C Brennan, L Chin, C Leo, M Kaur, P Zhu, M Rook, JL Wolfe, GM Makrigiorgos. Genome research, 2004, Nov, , 14(11): 2357-66. PMID: 15520297  |                            |
| 2  | <a href="#">Evaluation of affinity-based genome-wide DNA methylation data: Effects of CoG density, amplification bias, and copy number variation.</a>   | Score: 92.15<br>Ratio:0.89 |
|    | MD Robinson, C Storzaker, AL Statham, MW Coolen, JZ Song, SS Nair, D Strbenac, TP Speed, SJ Clark. Genome research, 2010, Dec, , 20(12): 1719-29. PMID: 21045081  |                            |
| 3  | <a href="#">Optical mapping discerns genome-wide DNA methylation profiles.</a>  | Score: 78.55<br>Ratio:0.76 |
|    | GE Ananiev, S Goldstein, R Runnheim, DK Forrest, S Zhou, K Potamouisis, CP Churas, V Bergendahl, JA Thomson, DC Schwartz. BMC molecular biology, 2008, , , 9(0): 68. PMID: 18667073   |                            |
| 4  | <a href="#">Isothermal whole genome amplification from single and small numbers of cells: a new era for preimplantation genetic diagnosis of inherited disease.</a>   | Score: 73.55<br>Ratio:0.71 |
|    | AH Handyside, MD Robinson, RJ Simpson, MB Omar, MA Shaw, JG Grudzinskas, A Rutherford. Molecular human reproduction, 2004, Oct, , 10(10): 767-72. PMID: 15322224  |                            |
| 5  | <a href="#">Whole genome amplification--applications and advances.</a>  | Score: 71.96<br>Ratio:0.69 |
|    | TL Hawkins, JC Detter, PM Richardson. Current opinion in biotechnology, 2002, Feb, , 13(1): 65-7. PMID: 11849960  |                            |
| 6  | <a href="#">Specific and complete human genome amplification with improved yield achieved by phi29 DNA polymerase and a novel primer at elevated temperature.</a>   | Score: 68.26<br>Ratio:0.66 |
|    | O Alsmadi, F Alkayal, D Monies, BF Meyer. BMC research notes, 2009, , , 2(0): 48. PMID: 19309528  |                            |
| 7  | <a href="#">HLA class II typing of whole genome amplified mouth swab DNA.</a>   | Score: 64.94<br>Ratio:0.62 |
|    | KM Gillespie, SJ Valovin, J Saunby, KM Hunter, DA Savage, D Middleton, JA Todd, PJ Bingley, EA Gale. Tissue antigens, 2000, Dec, , 56(6): 530-8. PMID: 11169243   |                            |
| 8  | <a href="#">Quantitative analysis of DNA methylation after whole bisulfite amplification of a minute amount of DNA from body fluids.</a>  | Score: 60.62<br>Ratio:0.58 |
|    | T Vaissière, C Cuenin, A Paliwal, P Vineis, G Hoek, M Krzyzanowski, L Airoidi, A Dunning, S Garte, P Hainaut, C Malaveille, K Overvad, F Clavel-Chapelon, J Linseisen, H Boeing, A Trichopoulou, D Trichopoulos, A Kaladidi, D Palli, V Krogh, R Tumino, S Panico, HB Bueno-De-Mesquita, PH Peeters, M Kumle, CA Gonzalez, C Martinez, M Dorronsoro, A Barricarte, C Navarro, JR Quiros, G Berglund, L Janzon, B Jarvholm, NE Day, TJ Key, R Saracci, R Kaaks, E Riboli, P Hainaut, Z Herczeg. Epigenetics : official journal of the DNA Methylation Society, 2009, May, , 4(4): 221-30. PMID: 19458486 |                            |
| 9  | <a href="#">Assessment of whole genome amplification-induced bias through high-throughput, massively parallel whole genome sequencing.</a>  | Score: 60.58<br>Ratio:0.58 |
|    | R Pinard, A de Winter, GJ Sarkis, MB Gerstein, KR Tartaro, RN Plant, M Egholm, JM Rothberg, JH Leamon. BMC genomics, 2006, , , 7(0): 216. PMID: 16928277  |                            |
| 10 | <a href="#">A whole-genome amplification protocol for a wide variety of DNAs, including those from formalin-fixed and paraffin-embedded tissue.</a>   | Score: 59.86<br>Ratio:0.58 |
|    | PL Paris. Methods in molecular biology (Clifton, N.J.), 2009, , , 556(0): 89-98. PMID: 19488873   |                            |
| 11 | <a href="#">[Perspective of DNA methylation in forensic genetics and new progress of its detection methods].</a>  | Score: 58.86<br>Ratio:0.57 |
|    | SM Zhao, CT Li. Fa yi xue za zhi, 2009, Aug, , 25(4): 290-5. PMID: 19788082   |                            |

Relevancy Threshold (Similarity ratio = 0.56). Entries above here have an unusual level of similarity

12	<a href="#">Methylation perturbations in retroelements within the genome of a Mus interspecific hybrid correlate with double minute chromosome formation.</a>	Score: 58.31 Ratio:0.56
	JD Brown, D Golden, RJ O'Neill. Genomics, 2008, Mar, , 91(3): 267-73. PMID: 18226492	
13	<a href="#">Evaluation of whole-genome amplification using multiple-displacement amplification of a limited number of cells.</a>	Score: 57.84 Ratio:0.56
	S Bashiardes, N Salame, PC Patsalis. Clinical chemistry and laboratory medicine : CCLM / FESCC, 2006, , , 44(9): 1158-60. PMID: 16958614	
14	<a href="#">Evaluation of whole genome amplification protocols for array and oligonucleotide CCH.</a>	Score: 57.27 Ratio:0.55
	A Hittelman, S Sridharan, R Roy, J Fridlyand, M Loda, C Collins, PL Paris. Diagnostic molecular pathology : the American journal of surgic, 2007, Dec, , 16(4): 198-206. PMID: 18043282	
15	<a href="#">Whole genome amplification of the rust Puccinia striiformis f. sp. tritici from single spores.</a>	Score: 56.54 Ratio:0.54
	Y Wang, M Zhu, R Zhang, H Yang, Y Wang, G Sun, S Jin, T Hsiang. Journal of microbiological methods, 2009, May, , 77(2): 229-34. PMID: 19233233	
16	<a href="#">A whole genome amplification method to generate long fragments from low quantities of genomic DNA.</a>	Score: 56.34 Ratio:0.54
	R Kittler, M Stoneking, M Kayser. Analytical biochemistry, 2002, Jan, , 300(2): 237-44. PMID: 11779116	
17	<a href="#">Whole genome amplification of sodium bisulfite-treated DNA allows the accurate estimate of methylated cytosine density in limited DNA resources.</a>	Score: 55.81 Ratio:0.54
	J Mill, S Yazdanpanah, E Gückel, S Ziegler, Z Kaminsky, A Petronis. BioTechniques, 2006, Nov, , 41(5): 603-7. PMID: 17140118	
18	<a href="#">Determining the global DNA methylation status of rat according to the identifier repetitive elements.</a>	Score: 55.81 Ratio:0.54
	HH Kim, JH Park, KS Jeong, S Lee. Electrophoresis, 2007, Nov, , 28(21): 3854-61. PMID: 17960839	
19	<a href="#">Profiling DNA methylation from small amounts of genomic DNA starting material: efficient sodium bisulfite conversion and subsequent whole-genome amplification.</a>	Score: 55.61 Ratio:0.53
	J Mill, A Petronis. Methods in molecular biology (Clifton, N.J.), 2009, , , 507(): 371-81. PMID: 18987828	
20	<a href="#">Analysis of DNA methylation by amplification of intermethylated sites (AIMS).</a>	Score: 54.05 Ratio:0.52
	M Jordà, J Rodríguez, J Frigola, MA Peinado. Methods in molecular biology (Clifton, N.J.), 2009, , , 507(): 107-16. PMID: 18987810	
21	<a href="#">Genome-wide divergence of DNA methylation marks in cerebellar and cerebellar cortices.</a>	Score: 53.68 Ratio:0.52
	Y Xin, B Chanrion, MM Liu, H Galfalvy, R Costa, B Ilievski, G Rosoklija, V Arango, AJ Dwork, JJ Mann, B Tycko, F Haghighi. PloS one, 2010, , , 5(6): e11357. PMID: 20596539	
22	<a href="#">SNP-based chromosomal copy number ascertainment following multiple displacement whole-genome amplification.</a>	Score: 53.67 Ratio:0.52
	JJ Corneveaux, MC Kruer, D Hu-Lince, KE Ramsey, VL Zismann, DA Stephan, DW Craig, MJ Huentelman. BioTechniques, 2007, Jan, , 42(1): 77-83. PMID: 17269488	
23	<a href="#">A genome-wide analysis of brain DNA methylation identifies new candidate genes for sporadic amyotrophic lateral sclerosis.</a>	Score: 53.39 Ratio:0.51
	JM Morahan, B Yu, RJ Trent, R Pamphlett. Amyotrophic lateral sclerosis : official publication of the Wor, , , 10(5-6): 418-29. PMID: 19922134	
24	<a href="#">Epigenetic profiling of the H12 differentially methylated region and comprehensive whole genome array-based analysis in Silver-Russell syndrome.</a>	Score: 53.36 Ratio:0.51
	SY Lin, CN Lee, CC Hung, WY Tsai, SP Lin, NC Li, WS Hsieh, YC Tung, DM Niu, WM Hsu, LY Chen, MY Fang, MP Tu, PW Kuo, CY Lin, YN Su, HN Ho. American journal of medical genetics. Part A, 2010, Oct, , 152A(10): 2521-8. PMID: 20830799	
25	<a href="#">The use of multiple displacement amplified DNA as a control for methylation specific PCR, pyrosequencing, bisulfite sequencing and methylation-sensitive restriction enzyme PCR.</a>	Score: 52.66 Ratio:0.51
	S Hughes, JL Jones. BMC molecular biology, 2007, , , 8(): 91. PMID: 17939862	
26	<a href="#">Mapping the genome landscape using tiling array technology.</a>	Score: 51.34 Ratio:0.49
	J Yazaki, BD Gregory, JR Ecker. Current opinion in plant biology, 2007, Oct, , 10(5): 534-42. PMID: 17703988	
27	<a href="#">Synthesis of universal unmethylated control DNA by nested whole genome amplification with phi29 DNA polymerase.</a>	Score: 51.27 Ratio:0.49
	N Umetani, MF de Maat, T Mori, H Takeuchi, DS Hoon. Biochemical and biophysical research communications, 2005, Apr, , 329(1): 219-23. PMID: 15721296	
28	<a href="#">GenoFree: software to design primers optimized for whole genome scanning by long-range PCR amplification.</a>	Score: 49.63 Ratio:0.48
	N Ben Zakour, M Gautier, R Andonov, D Lavenier, MF Cochet, P Veber, A Sorokin, Y Le Loir. Nucleic acids research, 2004, , , 32(1): 17-24. PMID: 14704339	
29	<a href="#">Mutations of TP53 induce loss of DNA methylation and amplification of the TROP1 gene.</a>	Score: 49.41 Ratio:0.48
	AF Nasr, M Nutini, B Palombo, E Guerra, S Alberti. Oncogene, 2003, Mar, , 22(11): 1668-77. PMID: 12642870	

- 30  [The vegetarian lifestyle and DNA methylation.](#) Score: 49.1  
Ratio:0.47  
J Geisel, H Schorr, M Bodis, S Isber, U Hübner, JP Knapp, R Obeid, W Herrmann. Clinical chemistry and laboratory medicine : CCLM / FESCC, 2005, , , 43(10): 1164-9. PMID: 16197315
- 31  [Two methods of whole-genome amplification enable accurate genotyping across a 2320-SNP linkage panel.](#) Score: 48.47  
Ratio:0.47  
DL Barker, MS Hansen, AF Faruqi, D Giannola, OR Irsula, RS Lasken, M Latterich, V Makarov, A Oliphant, JH Pinter, R Shen, I Sleptsova, W Ziehl, E Lai. Genome research, 2004, May, , 14(5): 901-7. PMID: 15123587
- 32  [Sequencing of the large dsDNA genome of Oryctes rhinoceros nudivirus using multiple displacement amplification of nanogram amounts of virus DNA.](#) Score: 47.45  
Ratio:0.46  
Y Wang, RG Kleespies, MB Ramle, JA Jehle. Journal of virological methods, 2008, Sep, , 152(1-2): 106-8. PMID: 18598718
- 33  [Whole genome amplification with Pfu29 DNA polymerase to enable genetic or genomic analysis of samples of low DNA yield.](#) Score: 46.96  
Ratio:0.45  
K Silander, J Saarela. Methods in molecular biology (Clifton, N.J.), 2008, , , 439(): 1-18. PMID: 18370092
- 34  [Whole genome amplification on polydimethylsiloxane microchip array.](#) Score: 45.11  
Ratio:0.43  
L Chen, A Manz, PJ Day. Analytical biochemistry, 2008, Jan, , 372(1): 128-30. PMID: 17949674
- 35  [Applications of DNA tiling arrays for whole-genome analysis.](#) Score: 44.51  
Ratio:0.43  
TC Mockler, S Chan, A Sundaresan, H Chen, SE Jacobsen, JR Ecker. Genomics, 2005, Jan, , 85(1): 1-15. PMID: 15607417
- 36  [Whole-genome multiple displacement amplification from single cells.](#) Score: 44.09  
Ratio:0.42  
C Spits, C Le Caignec, M De Rycke, L Van Haute, A Van Steirteghem, I Liebaers, K Sermon. Nature protocols, 2006, , , 1(4): 1965-70. PMID: 17487184
- 37  [Restriction landmark genome scanning.](#) Score: 43.53  
Ratio:0.42  
JF Costello, DJ Smiraglia, C Plass. Methods (San Diego, Calif.), 2002, Jun, , 27(2): 144-9. PMID: 12095273
- 38  [\[New molecular indicators for the prevention of tumor and degenerative diseases: anomalous DNA methylation\].](#) Score: 42.47  
Ratio:0.41  
G De Palma, P Mozzoni. Giornale italiano di medicina del lavoro ed ergonomia, , , 31(1): 51-3. PMID: 19558040
- 39  [Genome-wide association of histone H3 lysine nine methylation with CHG DNA methylation in Arabidopsis thaliana.](#) Score: 42.36  
Ratio:0.41  
YV Bernatavichute, X Zhang, S Cokus, M Pellegrini, SE Jacobsen. PloS one, 2008, , , 3(9): e3156. PMID: 18776934
- 40  [Whole genome amplification and de novo assembly of single bacterial cells.](#) Score: 41.22  
Ratio:0.4  
S Rodrigue, RR Malmstrom, AM Berlin, BW Birren, MR Henn, SW Chisholm. PloS one, 2009, , , 4(9): e6864. PMID: 19724646
- 41  [Highly efficient PCR assay to discriminate allelic DNA methylation status using whole genome amplification.](#) Score: 41.18  
Ratio:0.4  
Y Yamada, T Ito. BMC research notes, 2011, , , 4(): 179. PMID: 21663670
- 42  [Evaluation of 3 methods of whole-genome amplification for subsequent metaphase comparative genomic hybridization.](#) Score: 41.17  
Ratio:0.4  
G Ng, I Roberts, N Coleman. Diagnostic molecular pathology : the American journal of surgic, 2005, Dec, , 14(4): 203-12. PMID: 16319690
- 43  [Detection and analysis of mitochondrial DNA deletions by whole genome PCR.](#) Score: 39.35  
Ratio:0.38  
CH Tengan, CT Moraes. Biochemical and molecular medicine, 1996, Jun, , 58(1): 130-4. PMID: 8809354
- 44  [Maize DNA-sequencing strategies and genome organization.](#) Score: 39.2  
Ratio:0.38  
RJ Okagaki, RL Phillips. Genome biology, 2004, , , 5(5): 223. PMID: 15128439
- 45  [Study of tissue-specific CpG methylation of DNA in extended genomic loci.](#) Score: 39.1  
Ratio:0.38  
TL Azhikina, ED Sverdlov. Biochemistry. Biokhimiia, 2005, May, , 70(5): 596-603. PMID: 15948713
- 46  [Whole genome amplification from a single cell: implications for genetic analysis.](#) Score: 39  
Ratio:0.37  
L Zhang, X Cui, K Schmitt, R Hubert, W Navidi, N Arnheim. Proceedings of the National Academy of Sciences of the United S, 1992, Jul, , 89(13): 5847-51. PMID: 1631067
- 47  [Whole genome amplification: abundant supplies of DNA from precious samples or clinical specimens.](#) Score: 37.59  
Ratio:0.36  
RS Lasken, M Egholm. Trends in biotechnology, 2003, Dec, , 21(12): 531-5. PMID: 14624861
- 48  [Fidelity of whole-genome amplification of blood spot DNA for HLA typing and SNP analyses.](#) Score: 37.59  
Ratio:0.36  
KK Singh, SA Spector. Clinical genetics, 2007, Aug, , 72(2): 156-9. PMID: 17661821
- 49  [Whole-genome amplification of DNA from residual cells left by incidental contact.](#) Score: 37.59  
Ratio:0.36

- KJ Sorensen, K Turteltaub, G Vrankovich, J Williams, AT Christian. Analytical biochemistry, 2004, Jan, , 324(2): 312-4. PMID: 14690700
- 50  Improved efficacy of whole genome amplification from bacterial cells. Score: 37.59  
Ratio:0.36  
YM Kwon, MM Cox. BioTechniques, 2004, Jul, , 37(1): 40, 42, 44. PMID: 15283198
- 51  Genome-wide, high-resolution DNA methylation profiling using bisulfite-mediated cytosine conversion. Score: 37.38  
Ratio:0.36  
J Reinders, C Delucinge Vivier, G Theiler, D Chollet, P Descombes, J Paszkowski. Genome research, 2008, Mar, , 18(3): 469-76. PMID: 18218979
- 52  Whole genome amplification of plasma-circulating DNA enables expanded screening for allelic imbalance in plasma. Score: 37.18  
Ratio:0.36  
J Li, L Harris, H Mamon, MH Kulke, WH Liu, P Zhu, G Mike Makrigiorgos. The Journal of molecular diagnostics : JMD, 2006, Feb, , 8(1): 22-30. PMID: 16436631
- 53  Amplification of bisulfite-converted DNA for genome-wide DNA methylation profiling. Score: 36.93  
Ratio:0.36  
J Reinders. Cold Spring Harbor protocols, 2009, Dec, , 2009(12): pdb.prot5342. PMID: 20150089
- 54  Genome-wide scans using archived neonatal dried blood spot samples. Score: 36.46  
Ratio:0.35  
MV Hollegaard, J Grauholm, A Børglum, M Nyegaard, B Nørgaard-Pedersen, T Ørntoft, PB Mortensen, C Wiuf, O Mors, M Didriksen, P Thorsen, DM Hougaard. BMC genomics, 2009, , 10(): 297. PMID: 19575812
- 55  Whole-genome amplification of oral rinse self-collected DNA in a population-based case-control study of breast cancer. Score: 36.46  
Ratio:0.35  
X Liang, A Trentham-Dietz, L Titus-Ernstoff, PA Newcomb, RA Welch, AA Hutchinson, JM Hampton, CB Sutcliffe, JL Haines, KM Egan. Cancer epidemiology, biomarkers prevention : a publication of, 2007, Aug, , 16(8): 1610-4. PMID: 17684135
- 56  Virtual genome scan: a tool for restriction landmark-based scanning of the human genome. Score: 36.39  
Ratio:0.35  
JM Rouillard, AE Erson, R Kuick, J Asakawa, K Wimmer, M Muleris, EM Petty, S Hanash. Genome research, 2001, Aug, , 11(8): 1453-9. PMID: 11483587
- 57  Multiply primed rolling-circle amplification method for the amplification of circular DNA viruses. Score: 36.06  
Ratio:0.35  
H Stevens, A Rector, M Van Ranst. Cold Spring Harbor protocols, 2010, Apr, , 2010(4): pdb.prot5415. PMID: 20360369
- 58  Study on application of the whole genome amplification in LCNI. Score: 35.74  
Ratio:0.34  
HG Zhou, C Zhang. Fa yi xue za zhi, 2006, Feb, , 22(1): 43-4, 47. PMID: 16524185
- 59  Brugia malayi: whole genome amplification for genomic characterization of filarial parasites. Score: 35.63  
Ratio:0.34  
SN McNulty, GJ Weil, M Heinz, SD Crosby, PU Fischer. Experimental parasitology, 2008, Jun, , 119(2): 256-63. PMID: 18359019
- 60  Detection of cytosine methylation and mapping of a gene influencing cytosine methylation in the genome of Citrus. Score: 34.38  
Ratio:0.33  
Q Cai, CL Guy, GA Moore. Genome / National Research Council Canada = Génom / Conseil na, 1996, Apr, , 39(2): 235-42. PMID: 8984000
- 61  Singleton birth after preimplantation genetic diagnosis for Huntington disease using whole genome amplification. Score: 34.34  
Ratio:0.33  
JF Chow, WS Yeung, EY Lau, ST Lam, T Tong, EH Ng, PC Ho. Fertility and sterility, 2009, Aug, , 92(2): 828.e7-10. PMID: 19515365
- 62  Rolling-circle amplification of viral DNA genomes using phi29 polymerase. Score: 34.04  
Ratio:0.33  
R John, H Müller, A Rector, M van Ranst, H Stevens. Trends in microbiology, 2009, May, , 17(5): 205-11. PMID: 19375325
- 63  Primer design for Whole Genome Amplification using genetic algorithms. Score: 33.69  
Ratio:0.32  
AE Png, KW Choo, CI Lee, SH Leong, OL Kon. In silico biology, 2006, , 6(6): 505-14. PMID: 17518761
- 64  Application of whole genome amplification and quantitative PCR for detection and quantification of spoilage yeasts in orange juice. Score: 33.14  
Ratio:0.32  
A Renard, P Gómez di Marco, M Egea-Cortines, J Weiss. International journal of food microbiology, 2008, Aug, , 126(1-2): 195-201. PMID: 18597878
- 65  DNA methylation and the functional organization of the nuclear compartment. Score: 31.57  
Ratio:0.3  
J Espada, M Esteller. Seminars in cell developmental biology, 2010, Apr, , 21(2): 238-46. PMID: 19892028
- 66  Whole genome amplification and genetic analysis after extraction of proteins from dried blood spots. Score: 30.07  
Ratio:0.29  
MV Hollegaard, KM Sørensen, HK Petersen, MB Arnardottir, B Nørgaard-Pedersen, P Thorsen, DM Hougaard. Clinical chemistry, 2007, Jun, , 53(6): 1161-2. PMID: 17517589
- 67  Self-priming arrest by modified random oligonucleotides facilitates the quality control of whole genome amplification. Score: 30.07  
Ratio:0.29  
I Brukner, B Paquin, M Belouchi, D Labuda, M Krajcinovic. Analytical biochemistry, 2005, Apr, , 339(2): 345-7. PMID: 15797576
- 68  Comparing whole-genome amplification methods and sources of biological samples for single-nucleotide polymorphism genotyping. Score: 30.07  
Ratio:0.29

	JW Park, TH Beaty, P Boyce, AF Scott, I McIntosh. Clinical chemistry, 2005, Aug, , 51(8): 1520-3. PMID: 16040848	
69	<a href="#">[Di-(2-ethylhexyl) phthalate increases the DNA methylation level of genomes in the mouse testis].</a> SD Wu, J Zhu, YS Li, LQ Gan, XG Yuan, MD Xu, GH Wei. Zhonghua nan ke xue = National journal of andrology, 2009, Oct, , 15(10): 876-81. PMID: 20112733	Score: 29.85 Ratio:0.29
70	<a href="#">Comprehensive human genome amplification using multiple displacement amplification.</a> FB Dean, S Hosono, L Fang, X Wu, AF Faruqi, P Bray-Ward, Z Sun, Q Zong, Y Du, J Du, M Driscoll, W Song, SF Kingsmore, M Egholm, RS Lasken. Proceedings of the National Academy of Sciences of the United S, 2002, Apr, , 99(8): 5261-6. PMID: 11959976	Score: 29.65 Ratio:0.29
71	<a href="#">Variable patterns of total DNA and rDNA methylation in animals.</a> AP Bird, MH Taggart. Nucleic acids research, 1980, Apr, , 8(7): 1485-97. PMID: 6253937	Score: 28.4 Ratio:0.27
72	<a href="#">Efficient isothermal amplification of the entire genome from single cells.</a> KV Schowalter, J Fredrickson, AR Thornhill. Methods in molecular medicine, 2007, , , 132(): 87-99. PMID: 17876078	Score: 27.8 Ratio:0.27
73	<a href="#">Whole genome amplification of single cells: mathematical analysis of FFP and tagged PCR.</a> F Sun, N Arnheim, MS Waterman. Nucleic acids research, 1995, Aug, , 23(15): 3034-40. PMID: 7659528	Score: 27.19 Ratio:0.26
74	<a href="#">Towards the analysis of the genomes of single cells: further characterisation of the multiple displacement amplification.</a> S Panelli, G Damiani, L Espen, G Micheli, V Sgaramella. Gene, 2006, May, , 372(): 1-7. PMID: 16564650	Score: 25.8 Ratio:0.25
75	<a href="#">A whole-genome mouse BAC microarray with 1-Mb resolution for analysis of DNA copy number changes by array comparative genomic hybridization.</a> YJ Chung, J Jonkers, H Kitson, H Fiegler, S Humphray, C Scott, S Hunt, Y Yu, I Nishijima, A Velds, H Holstege, N Carter, A Bradley. Genome research, 2004, Jan, , 14(1): 188-96. PMID: 14707179	Score: 25.05 Ratio:0.24
76	<a href="#">Whole-genome allelotyping using laser microdissected tissue.</a> CM Feltmate, SC Mok. Methods in molecular biology (Clifton, N.J.), 2005, , , 293(): 69-77. PMID: 16028411	Score: 24.65 Ratio:0.24
77	<a href="#">BSMAF: whole genome bisulfite sequence MAFping program.</a> Y Xi, W Li. BMC bioinformatics, 2009, , , 10(): 232. PMID: 19635165	Score: 23.99 Ratio:0.23
78	<a href="#">[The amplification and high efficient cloning of the whole genome sequence of hepatitis B virus].</a> BY Xu, YM Wang, L Lang, YP Huang. Zhonghua gan zang bing za zhi = Zhonghua ganzangbing zazhi = Ch, 2005, Sep, , 13(9): 704-6. PMID: 16174469	Score: 23.48 Ratio:0.23
79	<a href="#">Preparation of genome-wide DNA fragment libraries using bisulfite in polyacrylamide gel electrophoresis slides with formamide denaturation and quality control for massively parallel sequencing by oligonucleotide ligation and detection.</a> SS Ranade, CB Chung, G Zon, VL Boyd. Analytical biochemistry, 2009, Jul, , 390(2): 126-35. PMID: 19379703	Score: 23.22 Ratio:0.22
80	<a href="#">Analysis and accurate quantification of CpG methylation by MALDI mass spectrometry.</a> J Tost, P Schatz, M Schuster, K Berlin, IG Gut. Nucleic acids research, 2003, May, , 31(9): e50. PMID: 12711695	Score: 21.96 Ratio:0.21
81	<a href="#">Preimplantation genetic diagnosis of Marfan syndrome using multiple displacement amplification.</a> B Lledó, J Ten, FM Galán, R Bernabeu. Fertility and sterility, 2006, Oct, , 86(4): 949-55. PMID: 17027361	Score: 21.62 Ratio:0.21
82	<a href="#">Evaluation of whole genome amplification methods using postmortem brain samples.</a> K Iwamoto, J Ueda, Y Nakano, M Bundo, W Ukai, E Hashimoto, T Saito, T Kato. Journal of neuroscience methods, 2007, Sep, , 165(1): 104-10. PMID: 17604841	Score: 21.57 Ratio:0.21
83	<a href="#">NotI subtraction and NotI-specific microarrays to detect copy number and methylation changes in whole genomes.</a> J Li, A Protopopov, F Wang, V Senchenko, V Petushkov, O Vorontsova, L Petrenko, V Zabarovska, O Muravenko, E Braga, L Kisselev, MI Lerman, V Kashuba, G Klein, I Ernberg, C Wahlestedt, ER Zabarovsky. Proceedings of the National Academy of Sciences of the United S, 2002, Aug, , 99(16): 10724-9. PMID: 12149436	Score: 21.46 Ratio:0.21
84	<a href="#">Genetic identity of clones and methods to explore DNA.</a> B de Montera, L Boulanger, S Taourit, JP Renard, A Eggen. Cloning and stem cells, 2004, , , 6(2): 133-9. PMID: 15268787	Score: 20.68 Ratio:0.2
85	<a href="#">Genome defense and DNA methylation in Neurospora.</a> EU Selker. Cold Spring Harbor symposia on quantitative biology, 2004, , , 69(): 119-24. PMID: 16117640	Score: 20.62 Ratio:0.2
86	<a href="#">Whole methylome analysis by ultra-deep sequencing using two-base encoding.</a> CA Bormann Chung, VL Boyd, KJ McKernan, Y Fu, C Monighetti, HE Peckham, M Barker. PloS one, 2010, , , 5(2): e9320. PMID: 20179767	Score: 20.57 Ratio:0.2
87	<a href="#">Amplifying whole insect genomes with multiple displacement amplification.</a>	Score: 19.93 Ratio:0.19

	N Gorrochotegui-Escalante, WC Black. Insect molecular biology, 2003, Apr, , 12(2): 195-200. PMID: 12653941	
88	<a href="#">Amplification of fungal genomes using multiple displacement amplification.</a> SJ Foster, BJ Monahan. Methods in molecular biology (Clifton, N.J.), 2010, , , 638(0): 175-85. PMID: 20238269	Score: 19.69 Ratio:0.19
89	<a href="#">Nonisotopic cytosine extension assay, a highly sensitive method to evaluate CpG island methylation in the whole genome.</a> H Fujiwara, M Ito. Analytical biochemistry, 2002, Aug, , 307(2): 386-9. PMID: 12202260	Score: 19.48 Ratio:0.19
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91	<a href="#">Methylome profiling of cancer cells by amplification of inter-methylated sites (AIMS).</a> J Frigola, M Ribas, RA Risques, MA Peinado. Nucleic acids research, 2002, Apr, , 30(7): e28. PMID: 11917034	Score: 18.53 Ratio:0.18
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94	<a href="#">Whole-genome disassembly.</a> P Green. Proceedings of the National Academy of Sciences of the United S, 2002, Apr, , 99(7): 4143-4. PMID: 11904394	Score: 14.85 Ratio:0.14
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98	<a href="#">Methylation matters: modeling a manageable genome.</a> JM Ordway, T Curran. Cell growth differentiation : the molecular biology journal o, 2002, Apr, , 13(4): 149-62. PMID: 11971815	Score: 10.12 Ratio:0.1
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